

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:03:19 ; Search time 103.636 Seconds
(without alignments)
74.117 Million cell updates/sec

Title: US-10-805-220-1

Perfect score: 77

Sequence: 1 QPVDQLKDLRNKPS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	132	Q9JGP3	Q9JGP3 borna disea
2	77	100.0	190	Q9IW59	Q9IW59 borna disea
3	77	100.0	201	VP24_BDV	P26668 borna disea
4	77	100.0	201	O10393	O10393 borna disea
5	77	100.0	201	O10402	O10402 borna disea
6	77	100.0	201	O10404	O10404 borna disea
7	77	100.0	201	O10405	O10405 borna disea
8	77	100.0	201	O10406	O10406 borna disea
9	77	100.0	201	Q91221	Q91221 borna disea
10	77	100.0	201	Q91228	Q91228 borna disea
11	77	100.0	201	Q65456	Q65456 borna disea
12	77	100.0	201	Q65457	Q65457 borna disea
13	77	100.0	201	Q65458	Q65458 borna disea
14	77	100.0	201	Q8BB28	Q8BB28 borna disea
15	77	100.0	201	Q9WRJ6	Q9WRJ6 borna disea
16	74	96.1	201	Q9Q9U9	Q9Q9U9 borna disea
17	74	96.1	201	Q64GK7	Q64GK7 borna disea
18	74	96.1	201	Q64GK9	Q64GK9 borna disea
19	74	96.1	202	Q64GK8	Q64GK8 borna disea
20	50	64.9	26	Q9QCJ3	Q9QCJ3 borna disea
21	50	64.9	26	Q9QCJ4	Q9QCJ4 borna disea
22	50	64.9	26	Q9QCJ5	Q9QCJ5 borna disea
23	50	64.9	26	Q9QCJ6	Q9QCJ6 borna disea
24	50	64.9	26	Q9QCJ7	Q9QCJ7 borna disea
25	50	64.9	26	Q9QCJ9	Q9QCJ9 borna disea
26	50	64.9	26	Q9QCK0	Q9QCK0 borna disea
27	50	64.9	147	Q77A24	Q77A24 borna disea
28	50	64.9	147	Q77A25	Q77A25 borna disea
29	50	64.9	147	Q77A26	Q77A26 borna disea
30	50	64.9	147	Q77A27	Q77A27 borna disea
31	50	64.9	147	Q77A28	Q77A28 borna disea

32	50	64.9	147	2	Q9W907	Q9W907 borna disea
33	50	64.9	147	2	Q9WN16	Q9WN16 borna disea
34	50	64.9	456	2	O7KZ78	O7KZ78 homo sapien
35	50	64.9	464	2	O43159	O43159 homo sapien
36	49.5	64.3	420	2	Q9XZ31	Q9XZ31 drosophila
37	48	62.3	451	2	Q8BHW3	Q8BHW3 mus musculus
38	48	62.3	457	2	Q9DB85	Q9DB85 m mus muscu
39	46	59.7	179	2	Q9KJVE	Q9KJVE salmonella
40	46	59.7	274	2	O32167	O32167 bacillus eu
41	46	59.7	466	1	FLID_SALTY	FLID_SALTY
42	46	59.7	467	2	Q8Z5S7	Q8Z5S7 salmonella
43	45	58.4	766	2	Q7PPE2	Q7PPE2 anopheles g
44	44	57.1	209	2	Q8N4U2	Q8N4U2 homo sapien
45	44	57.1	236	2	Q71XN1	Q71XN1 listeria mo

ALIGNMENTS

RESULT 1

Q9JGP3	PRELIMINARY;	PRT;	132 AA.
AC	Q9JGP3		
DT	01-OCT-2000 (Tremblrel. 15, Created)		
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	P24 (Fragment).		
OS	Borna disease virus (BDV).		
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;		
OC	Bornavirus.		
OX	NCBI_TaxID=12455;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20321452; PubMed=10861642;		
RX	DOI=10.1002/1096-9071(200007)61:3<336::AID-JMV9-3.3.CO;2-G;		
RA	Tsuji K., Toyomatsu K., Imamura Y., Maeda H., Toyoda T.;		
RT	"No association of borna disease virus with psychiatric disorders		
RT	among patients in northern Kyushu, Japan.";		
RL	J. Med. Virol. 61:336-340(2000).		
DR	EMBL; AB030740; BAA93477.1; -		
DR	InterPro; IPR009517; BDV_P24.		
DR	Pfam; PF06595; BDV_P24; 1.		
FT	NON_TER 1		
FT	NON_TER 132		
SQ	SEQUENCE 132 AA; 14894 MW; BA80E8F6D802FF93 CRC64;		

Query Match 100.0%; Score 77; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QPVDQLKDLRNKPS 15
Db	7	QPVDQLKDLRNKPS 21

RESULT 2

Q9IW59	PRELIMINARY;	PRT;	190 AA.
AC	Q9IW59		
DT	01-OCT-2000 (Tremblrel. 15, Created)		
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	Phosphoprotein (Fragment).		
GN	Name=P24;		
OS	Borna disease virus (BDV).		
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;		
OC	Bornavirus.		
OX	NCBI_TaxID=12455;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ratBDV;		
RX	MEDLINE=20086019; PubMed=10622306; DOI=10.1016/S0140-6736(99)04703-0;		
RA	Schwemmler M., Jehle C., Formella S., Staeheli P.;		

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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:18:12 ; Search time 22.2727 Seconds
(without alignments)
64.799 Million cell updates/sec

Title: US-10-805-220-1

Perfect score: 77

Sequence: 1 QPVDQLKDLRKNS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	77	2	JQ1295
2	77	100.0	201	1	WMVVD
3	77	100.0	201	2	24K antigen - born
4	46	59.7	274	2	probable structure
5	46	59.7	467	2	conserved hypotet
6	46	59.7	467	2	flagellar hook ass
7	44	57.1	243	2	hypothetical prote
8	44	57.1	539	2	flagellar hook-ass
9	43	55.8	386	1	hypothetical prote
10	43	55.8	488	2	fumarate hydratase
11	43	55.8	664	2	histidine decarbox
12	43	55.8	895	1	hypothetical prote
13	43	55.8	2475	2	hevin precursor -
14	42	54.5	445	2	H+-exporting Atlas
15	42	54.5	1075	2	polyprotein pp220
16	42	54.5	1075	2	cytochrome P450 -
17	41	53.2	129	2	Exportin1 (Xpo1) p
18	41	53.2	141	2	exportin 1 (valida
19	41	53.2	435	2	hypothetical prote
20	41	53.2	448	2	acetyl transferase
21	41	53.2	474	2	chaperonin 60 beta
22	41	53.2	491	2	probable carboxyl-
23	41	53.2	556	2	hypothetical prote
24	41	53.2	556	2	probable glucosyl
25	41	53.2	556	2	probable dnaK prot
26	41	53.2	556	2	probable dnaK-type
27	40	51.9	79	2	probable fad10 pr
28	40	51.9	213	2	type III secretion
29	40	51.9	218	2	cell division prot
					hypothetical prote

exodeoxyribonuclea
probable cyctathio
hypothetical prote
phosphomannomutase
aromatic-L-amino-a
NAD ADP-riboosyltra
interphotoreceptor
hypothetical prote
Taxi-binding prote
beta-phosphoglucom
thymidylate syntha
2'-hydroxyisoflavo
hypothetical prote
carbonate dehydrat
probable membrane,

ALIGNMENTS

RESULT 1

JQ1295

hypothetical 8.8K protein - borna disease virus

N:Alternate names: ORF S protein

C:Species: borna disease virus

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: JQ1295

R:Richt, J.A.; Vandewoude, S.; Zink, M.C.; Narayan, O.; Clements, J.E.

J. Gen. Virol. 72, 2251-2255, 1991

A:Title: Analysis of Borna disease virus-specific RNAs in infected cells and tissues.

A:Reference number: JQ1294; MUID:91374026; PMID:1895063

A:Accession: JQ1295

A:Molecule type: genomic RNA

A:Residues: 1-77 <RIC>

A:Cross-references: UNIPROT:P26668

C:Comment: Borna disease virus is an infectious agent that causes profound disturbances

C:Superfamily: borna disease virus 24K antigen

C:Keywords: nucleus

Query Match 100.0%; Score 77; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPVDQLKDLRKNS 15

DB 41 QPVDQLKDLRKNS 55

RESULT 2

WMVVD

24K antigen - borna disease virus

C:Species: borna disease virus

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Aug-2004

C:Accession: JQ1407; PQ0279; S15568

R:Thierer, J.; Riehle, H.; Grebenstein, O.; Binz, T.; Herzog, S.; Thiedenmann, N.; Stitz,

J. Gen. Virol. 73, 413-416, 1992

A:Title: The 24K protein of Borna disease virus.

A:Reference number: JQ1407; MUID:92166750; PMID:1538196

A:Accession: JQ1407

A:Molecule type: mRNA

A:Residues: 1-201 <TH1>

A:Cross-references: UNIPROT:P26668; EMBL:X60701; NID:G60640; PIDN:CAA43112.1; PID:G60641

A:Accession: PQ0279

A:Molecule type: protein

A:Residues: 37-44;77-89;95-103;133-139;159-167 <TH2>

C:Superfamily: Borna disease virus 24K antigen

Query Match 100.0%; Score 77; DB 1; Length 201;

Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPVDQLKDLRKNS 15

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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:01:59 ; Search time 112.273 Seconds
(without alignments)
51.672 Million cell updates/sec

Title: US-10-805-220-1

Perfect score: 77

Sequence: 1 QPVDQLLRKPS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A_Geneseq_16Dec04:*
- 2: Geneseqp1980s:*
- 3: Geneseqp1990s:*
- 4: Geneseqp2000s:*
- 5: Geneseqp2001s:*
- 6: Geneseqp2002s:*
- 7: Geneseqp2003as:*
- 8: Geneseqp2003bs:*
- 9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	15	ADQ39906	Borna dis
2	77	100.0	201	AAR98618	Borna dis
3	77	100.0	201	AAR98618	Borna dis
4	77	100.0	201	AAR98618	Borna dis
5	77	100.0	201	AAR98618	Borna dis
6	50	64.9	456	AAR98618	Borna dis
7	50	64.9	456	AAR98618	Borna dis
8	50	64.9	456	AAR98618	Borna dis
9	50	64.9	456	AAR98618	Borna dis
10	49.5	64.3	420	ABM81223	Tumour-as
11	44	57.1	140	ABM81223	Tumour-as
12	44	57.1	243	ABM81223	Tumour-as
13	44	57.1	860	ABM81223	Tumour-as
14	44	57.1	860	ABM81223	Tumour-as
15	44	57.1	1386	ABM81223	Tumour-as
16	44	57.1	1427	ABM81223	Tumour-as
17	43	55.8	213	ABP43212	Human ova
18	43	55.8	664	ABP43212	Human ova
19	43	55.8	664	ABP43212	Human ova
20	43	55.8	664	ABP43212	Human ova
21	43	55.8	664	ABP43212	Human ova
22	43	55.8	664	ABP43212	Human ova
23	43	55.8	664	ABP43212	Human ova
24	43	55.8	664	ABP43212	Human ova
25	43	55.8	664	ABP43212	Human ova

26	43	55.8	664	8	ADQ39906	Human myo
27	43	55.8	664	8	ADQ39906	Human myo
28	43	55.8	664	8	ADQ39906	Human myo
29	43	55.8	664	3	ADQ39906	Human myo
30	43	55.8	664	3	ADQ39906	Human myo
31	43	55.8	664	3	ADQ39906	Human myo
32	43	55.8	664	3	ADQ39906	Human myo
33	43	55.8	664	3	ADQ39906	Human myo
34	43	55.8	664	3	ADQ39906	Human myo
35	43	55.8	664	3	ADQ39906	Human myo
36	43	55.8	664	3	ADQ39906	Human myo
37	43	55.8	664	3	ADQ39906	Human myo
38	43	55.8	664	3	ADQ39906	Human myo
39	43	55.8	664	3	ADQ39906	Human myo
40	43	55.8	664	3	ADQ39906	Human myo
41	43	55.8	664	3	ADQ39906	Human myo
42	43	55.8	664	3	ADQ39906	Human myo
43	43	55.8	664	3	ADQ39906	Human myo
44	43	55.8	664	3	ADQ39906	Human myo
45	43	55.8	664	3	ADQ39906	Human myo

ALIGNMENTS

RESULT 1

ADQ39906

ID ADQ39906 standard; peptide; 15 AA.

XX ADQ39906

XX 02-DEC-2004 (first entry)

XX Borna disease virus p24 protein fragment for detecting BDV infections.

XX detection; exogenous antigen; class switching; IgM; IgG; immunoglobulin;

XX BDV; Borna disease virus; p24.

XX Borna disease virus.

XX EP1460426-A1.

XX 22-SEP-2004.

XX 19-MAR-2004; 2004EP-00006699.

XX 20-MAR-2003; 2003JP-00078898.

XX 26-MAR-2003; 2003JP-00086490.

XX 26-MAR-2003; 2003JP-00086491.

XX (SYSM-) SYSMEX CORP.

XX Yamaguchi K, Horii Y, Takahama Y, Nagai S;

XX WPI; 2004-679696/67.

XX Detecting antibody against exogenous antigen e.g. Borna disease virus

XX (BDV), involves detecting the IgM antibody to the exogenous antigen.

XX Claim 13; SEQ ID NO 1; 33pp; English.

XX The invention relates to a method of detecting (M1) an antibody, where an

XX examination of a disease caused by an exogenous antigen is conducted, the

XX exogenous antigen being an antigen having a property in which the class

XX switching from the IgM antibody to the IgG antibody of immunoglobulin

XX antibodies raised against the antigen is achieved after two months

XX following the appearance of the IgM antibody, the method involves

XX detecting the IgM antibody to the exogenous antigen. The method involves

XX also disclosing a reagent (1) for detecting an anti-BDV antibody, CC

XX comprising an antigen polypeptide selected from the p10 region of a Borna

XX disease virus (BDV) protein. (M1) is useful for detecting an antibody

XX specific to an exogenous antigen. The exogenous antigen is a

XX microorganism, virus and/or proteinaceous substance, which may be the

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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:27:58 ; Search time 123.818 Seconds
(without alignments)
60.826 Million cell updates/sec

Title: US-10-805-220-3
Perfect score: 94
Sequence: 1 PRRRLVDDADAMEDQDLY 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	18	16 US-10-805-220-3	Sequence 3, Appl1
2	83	88.3	18	16 US-10-627-141-39	Sequence 39, Appl
3	48	51.1	167	20 US-11-097-143-32475	Sequence 32475, A
4	46	48.9	131	9 US-09-989-722-276	Sequence 276, App
5	46	48.9	131	9 US-09-989-723-276	Sequence 276, App
6	46	48.9	131	9 US-09-989-279-276	Sequence 276, App
7	46	48.9	131	9 US-09-989-727-276	Sequence 276, App
8	46	48.9	131	9 US-09-989-731-276	Sequence 276, App
9	46	48.9	131	9 US-09-989-732-276	Sequence 276, App
10	46	48.9	131	9 US-09-991-073-276	Sequence 276, App
11	46	48.9	131	9 US-09-990-442-276	Sequence 276, App

12	46	48.9	131	9	US-09-991-163-276	Sequence 276, App
13	46	48.9	131	9	US-09-993-604-276	Sequence 276, App
14	46	48.9	131	9	US-09-990-456-276	Sequence 276, App
15	46	48.9	131	9	US-09-989-721-276	Sequence 276, App
16	46	48.9	131	9	US-09-992-598-276	Sequence 276, App
17	46	48.9	131	9	US-09-989-293A-276	Sequence 276, App
18	46	48.9	131	9	US-09-989-735-276	Sequence 276, App
19	46	48.9	131	9	US-09-990-444-276	Sequence 276, App
20	46	48.9	131	9	US-09-991-181-276	Sequence 276, App
21	46	48.9	131	9	US-09-989-730-276	Sequence 276, App
22	46	48.9	131	9	US-09-990-436-276	Sequence 276, App
23	46	48.9	131	9	US-09-993-687-276	Sequence 276, App
24	46	48.9	131	10	US-09-989-734-276	Sequence 276, App
25	46	48.9	131	10	US-09-997-653-276	Sequence 276, App
26	46	48.9	131	10	US-09-989-724-276	Sequence 276, App
27	46	48.9	131	10	US-09-989-728-276	Sequence 276, App
28	46	48.9	131	10	US-09-990-441-276	Sequence 276, App
29	46	48.9	131	10	US-09-993-667-276	Sequence 276, App
30	46	48.9	131	10	US-09-997-428-276	Sequence 276, App
31	46	48.9	131	10	US-09-997-666-276	Sequence 276, App
32	46	48.9	131	10	US-09-990-438-276	Sequence 276, App
33	46	48.9	131	10	US-09-990-562-276	Sequence 276, App
34	46	48.9	131	10	US-09-990-711-276	Sequence 276, App
35	46	48.9	131	10	US-09-989-726-276	Sequence 276, App
36	46	48.9	131	10	US-09-998-156-276	Sequence 276, App
37	46	48.9	131	10	US-09-990-437-276	Sequence 276, App
38	46	48.9	131	10	US-09-991-157-276	Sequence 276, App
39	46	48.9	131	10	US-09-997-514-276	Sequence 276, App
40	46	48.9	131	10	US-09-997-573-276	Sequence 276, App
41	46	48.9	131	10	US-09-991-172-276	Sequence 276, App
42	46	48.9	131	10	US-09-990-726-276	Sequence 276, App
43	46	48.9	131	10	US-09-997-559-276	Sequence 276, App
44	46	48.9	131	10	US-09-997-601-276	Sequence 276, App
45	46	48.9	131	10	US-09-990-443-276	Sequence 276, App

ALIGNMENTS

RESULT 1
US-10-805-220-3
; Sequence 3, Application US/10805220
; Publication NO. US20040234955A1
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, Kazunari
; APPLICANT: HORII, Yoichi
; APPLICANT: TAKAHAMA, Youichi
; APPLICANT: NAGAI, Shinya
; TITLE OF INVENTION: METHOD FOR DETECTING ANTIBODY AND ANTIGEN FOR DETECTING BORNA
; TITLE OF INVENTION: DISEASE VIRUS
; FILE REFERENCE: Q80490
; CURRENT APPLICATION NUMBER: US/10/805,220
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: JPA 2003-078898
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JPA 2003-086490
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: JPA 2003-086491
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Borna disease virus
US-10-805-220-3

Query Match 100.0%; Score 94; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PRRRLVDDADAMEDQDLY 18
|||||

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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:21:48, Search time 33.2727 Seconds
(without alignments)
40.384 Million cell updates/sec

Title: US-10-805-220-3

Perfect score: 94

Sequence: 1 PKRLVDDADAMEDQDLY 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A COMB.pcp:*
2: /cgn2_6/prodata/1/1aa/5B COMB.pcp:*
3: /cgn2_6/prodata/1/1aa/6A COMB.pcp:*
4: /cgn2_6/prodata/1/1aa/6B COMB.pcp:*
5: /cgn2_6/prodata/1/1aa/PCTUS COMB.pcp:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	370	US-08-369-822C-2	Sequence 2, Appli
2	94	100.0	370	US-08-582-776C-2	Sequence 2, Appli
3	94	100.0	370	US-08-434-831B-2	Sequence 2, Appli
4	83	88.3	18	US-08-779-764A-39	Sequence 39, Appl
5	83	88.3	18	US-09-563-456-39	Sequence 39, Appl
6	46	48.9	131	US-09-839-709-2	Sequence 2, Appli
7	43.5	46.3	314	US-08-989-478-4	Sequence 4, Appli
8	43.5	46.3	314	US-08-996-685-4	Sequence 4, Appli
9	43	45.7	444	US-09-583-110-2893	Sequence 2893, Ap
10	43	45.7	469	US-09-107-433-3766	Sequence 3766, Ap
11	43	45.7	481	US-09-489-039A-10323	Sequence 10323, A
12	43	45.7	1083	US-09-538-092-419	Sequence 419, App
13	43	45.7	1881	US-09-233-086-3	Sequence 3, Appli
14	43	43.6	291	US-09-252-991A-25517	Sequence 25517, A
15	41	43.6	413	US-09-134-000C-6481	Sequence 6481, Ap
16	41	43.6	1066	US-09-252-991A-31530	Sequence 31530, A
17	41	43.6	1136	US-09-252-991A-31394	Sequence 31394, A
18	40	42.6	81	US-09-513-999C-4764	Sequence 4764, Ap
19	40	42.6	105	US-09-198-452A-406	Sequence 406, App
20	40	42.6	107	US-09-513-999C-6047	Sequence 6047, Ap
21	40	42.6	151	US-09-621-976-4660	Sequence 4660, Ap
22	40	42.6	166	US-09-438-185A-388	Sequence 388, App
23	40	42.6	197	US-09-248-796A-23752	Sequence 23752, A
24	40	42.6	258	US-09-248-796A-18803	Sequence 18803, A
25	40	42.6	265	US-09-538-092-751	Sequence 751, App
26	40	42.6	383	US-08-484-575A-4	Sequence 4, Appli
27	40	42.6	383	US-08-477-459-4	Sequence 4, Appli

28	40	42.6	383	3	US-08-479-869-4	Sequence 4, Appli
29	40	42.6	383	3	US-08-486-414-4	Sequence 4, Appli
30	40	42.6	383	5	PCT-US94-01826A-4	Sequence 4, Appli
31	40	42.6	383	5	PCT-US94-02252A-4	Sequence 4, Appli
32	40	42.6	395	4	US-09-949-016-8564	Sequence 8564, Ap
33	40	42.6	429	4	US-09-248-796A-14642	Sequence 14642, A
34	40	42.6	544	4	US-09-248-796A-18637	Sequence 18637, A
35	40	42.6	895	4	US-09-538-092-1158	Sequence 1158, Ap
36	40	42.6	909	4	US-09-976-594-324	Sequence 324, App
37	40	42.6	4861	4	US-09-919-497-70	Sequence 70, Appl
38	39.5	42.0	22	2	US-08-802-322-11	Sequence 11, Appl
39	39.5	42.0	22	4	US-09-832-161-11	Sequence 11, Appl
40	39.5	42.0	314	2	US-08-989-478-3	Sequence 3, Appli
41	39.5	42.0	314	3	US-08-996-685-3	Sequence 3, Appli
42	39.5	42.0	347	2	US-08-802-322-13	Sequence 13, Appl
43	39.5	42.0	347	4	US-09-832-161-13	Sequence 13, Appl
44	39	41.5	173	4	US-09-602-787A-210	Sequence 210, App
45	39	41.5	237	4	US-09-602-777A-310	Sequence 310, App

ALIGNMENTS

RESULT 1
US-08-369-822C-2
Sequence 2, Application US/08369822C
Patent No. 6015660
GENERAL INFORMATION:
APPLICANT: Lipkin, W. I.
APPLICANT: Biese, Thomas
APPLICANT: Klische, Stefanie
APPLICANT: Schneider, Patrick A.
APPLICANT: Stitz, Lothar
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borna Disease Viral Sequences,
TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017-2571
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,822C
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Churchill, Margaret A. (Ph.D.)
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279-194XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/892-9200
TELEFAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-369-822C-2

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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:03:19 ; Search time 124.364 Seconds
(without alignments)
74.117 Million cell updates/sec

Title: US-10-805-220-3

Perfect score: 94

Sequence: 1 FKRRLVDDADAMEDQDLY 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	370	1 VP40 BDV	Q01552 borna disea
2	94	100.0	370	2 O10392	O10392 borna disea
3	94	100.0	370	2 O10395	O10395 borna disea
4	94	100.0	370	2 O10398	O10398 borna disea
5	94	100.0	370	2 O10401	O10401 borna disea
6	94	100.0	370	2 Q910H1	Q910H1 borna disea
7	94	100.0	370	2 Q91UL4	Q91UL4 borna disea
8	94	100.0	370	2 Q91UL8	Q91UL8 borna disea
9	94	100.0	370	2 Q8BB29	Q8BB29 borna disea
10	77.5	82.4	369	2 Q9Q9V1	Q9Q9V1 borna disea
11	54	57.4	947	2 Q9P449	Q9P449 schizophyll
12	49	52.1	944	2 Q7SE56	Q7SE56 neurospora
13	48.5	51.6	130	2 Q7XBG3	Q7XBG3 setaria ita
14	48	51.1	167	2 Q9V506	Q9V506 drosophila
15	47	50.0	252	2 Q89P43	Q89P43 bradyrhizob
16	47	50.0	441	2 Q8SEV2	Q8SEV2 guillardia
17	47	50.0	824	2 Q9SY82	Q9SY82 arabidopsis
18	46	48.9	131	1 LEU1_HUMAN	Q95214 homo sapien
19	46	48.9	131	1 LEU1_MOUSE	Q95214 mus musculu
20	46	48.9	131	2 Q6PDU4	Q6PDU4 rattus norv
21	45.5	48.4	527	2 Q94IX9	Q94IX9 oryza sativ
22	45	47.9	198	2 Q9H791	Q9H791 homo sapien
23	45	47.9	304	2 Q8SUA7	Q8SUA7 encephalito
24	45	47.9	647	2 Q8IZM8	Q8IZM8 homo sapien
25	44	47.9	937	2 Q86L47	Q86L47 dictyosteli
26	44	46.8	156	2 Q665T9	Q665T9 versinia ps
27	44	46.8	156	2 Q82I75	Q82I75 versinia pe
28	44	46.8	170	2 Q8CKF8	Q8CKF8 versinia pe
29	44	46.8	285	2 Q8P7I9	Q8P7I9 xanthomonas
30	44	46.8	286	2 Q8P7W2	Q8P7W2 xanthomonas
31	44	46.8	404	2 Q7PYV1	Q7PYV1 anopheles g

32	44	46.8	507	2 Q8X390	Q8X390 mus musculu
33	44	46.8	571	2 Q9DAU9	Q9DAU9 mus musculu
34	44	46.8	588	2 Q6GV68	Q6GV68 ctenopharyn
35	44	46.8	639	2 Q9SGH6	Q9SGH6 arabidopsis
36	44	46.8	842	2 Q9U0J9	Q9U0J9 plasmodium
37	44	46.8	2304	1 YCF2_AMBTC	P61341 amborella t
38	43.5	46.3	314	1 IKBA_RAT	Q63746 rattus norv
39	43	45.7	209	2 Q98KY1	Q98KY1 rhizobium l
40	43	45.7	226	2 Q7Y4L7	Q7Y4L7 streptococc
41	43	45.7	251	2 Q7X3I6	Q7X3I6 franciella
42	43	45.7	444	2 Q97551	Q97551 streptococc
43	43	45.7	553	2 Q8LTY0	Q8LTY0 bacterioph
44	43	45.7	613	2 Q8BDD7	Q8BDD7 bovine papi
45	43	45.7	716	2 Q7SF63	Q7SF63 neurospora

ALIGNMENTS

RESULT 1
ID VP40 BDV STANDARD; PRT; 370 AA.
AC Q01552;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 40 kDa protein.
GN Name=P40; Synonyms=P38;
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RA MEDLINE=94149825; PubMed=7906311;
RX Cubitt B., Oldstone C., de la Torre J.C.;
RT "Sequence and genome organization of Borna disease virus.";
RL J. Virol. 68:1382-1396(1994).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Clone B8;
RX MEDLINE=93303922; PubMed=8317098;
RA Pyper J.M., Richt J.A., Brown L., Rott R., Narayan O., Clements J.E.;
RT "Genomic organization of the structural proteins of borna disease virus revealed by a cDNA clone encoding the 38-kDa protein.";
RL Virology 195:229-238(1993).
RN [3]
RP SEQUENCE OF 10-370 FROM N.A.
RC STRAIN=Giessen / HE/80-3;
RA Binz T., Riehle H., Yamasaki J., Richt J.A., Grebenstein O., Rott R.,
RL Niemann H.;
RT Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Halle B1/91;
RX MEDLINE=94076462; PubMed=8254777;
RA Schneider P.A., Briese T., Zimmermann W., Ludwig H., Lipkin W.I.;
RT "Sequence conservation in field and experimental isolates of Borna disease virus.";
RL J. Virol. 68:63-68(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=V;
RX MEDLINE=94240137; PubMed=8183914;
RA Briese T., Schneemann A., Lewis A.J., Park Y.-S., Kim S., Ludwig H.,
RL Lipkin W.I.;
RT "Genomic organization of Borna disease virus.";
RN [6]
RP Proc. Natl. Acad. Sci. U.S.A. 91:4362-4366(1994).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=HE/80-1;
RX MEDLINE=93021385; PubMed=1404604;

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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:18:12 ; Search time 26.7273 Seconds
(without alignments)
64.799 Million cell updates/sec

Title: US-10-805-220-3
Perfect score: 94
Sequence: 1 PKRLVDDADAMEDQDLY 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	370	2 A49528	probable structural component p40 - borna disease virus
2	47	50.0	441	2 E90136	tubulin beta subunit
3	44	46.8	156	2 AB0079	hypothetical prote
4	43.5	46.3	314	2 A44437	regenerating liver
5	43	45.7	444	2 E95065	conserved hypothet
6	43	45.7	1083	2 S88460	probable membrane
7	42.5	45.2	919	2 C87445	DNA gyrase subunit
8	42	44.7	389	2 T03691	calreticulin - com
9	42	44.7	416	2 T16968	calreticulin call
10	42	44.7	447	2 T46146	hypothetical prote
11	42	44.7	812	2 T34180	hypothetical prote
12	42	44.7	813	2 C97292	Atfases with chape
13	42	44.7	1287	2 T22235	hypothetical prote
14	41	43.6	229	1 MFVNUJ	matrix protein - v
15	41	43.6	266	2 E84292	extragenic suppres
16	41	43.6	277	2 G69158	conserved hypothet
17	41	43.6	284	2 E97216	probable aminoglyc
18	41	43.6	301	2 E98811	hypothetical prote
19	41	43.6	358	2 S30603	N5,N10-methylene
20	41	43.6	369	2 H70650	hypothetical prote
21	41	43.6	411	2 H83355	hypothetical prote
22	41	43.6	444	2 P97932	conserved hypothet
23	41	43.6	519	2 D82522	type I restriction
24	41	43.6	526	2 A86440	58.5K hypothetical
25	41	43.6	902	2 T00072	hypothetical prote
26	40.5	43.1	524	2 C81367	phosphoenolpyruvat
27	40.5	43.1	567	2 S50708	hexose transport p
28	40.5	43.1	681	2 T19482	hypothetical prote
29	40	42.6	127	2 T16131	hypothetical prote

single-strand bind
ss DNA binding pro
cerbellar degener
probable magnesium
hypothetical prote
transcription fact
hypothetical prote
acetylglutamate sy
alpha-amyase a pr
hypothetical prote
DNA mismatch repai
F9L1 24 protein -
hypothetical prote
replication licens
hypothetical prote

ALIGNMENTS

RESULT 1

A49528
probable structural component p40 - borna disease virus
N:Alternate names: 39K antigen
C:Species: borna disease virus
C>Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text_change 28-Jul-2000
A:Accession: A49528; A37475; S25642; A44004
R:Schneider, P.A.; Briese, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.
J Virol. 68, 63-68, 1994
A>Title: Sequence conservation in field and experimental isolates of Borna disease vir
A:Reference number: A49528; MUID:94076462; PMID:8254777
A:Accession: A49528
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-370 <SCH>
A:Cross-references: GB:S67502; NID:9456883; PIDN:AA829214.1; PID:9456886
A:Experimental source: WI-1, Halle BI/91, horse brain, field isolate
A>Note: sequence extracted from NCBI backbone (NCBIN:141399, NCBIP:141401)
R:Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.E.
Virology 195, 229-238, 1993
A>Title: Genomic organization of the structural proteins of borna disease virus reveal
A:Reference number: A37475; MUID:93303922; PMID:8317098
A:Accession: A37475
A:Molecule type: mRNA
A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>
A:Cross-references: GB:S62821; NID:9386390; PIDN:AA827261.1; PID:9386391
A>Note: sequences extracted from NCBI backbone (NCBIN:134146, NCBIP:134147)
A>Note: parts of this sequence were confirmed by peptide sequencing
R:Binz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,
submitted to the EMBL Data Library, September 1992
A:Description: The 39/39k antigen of borna disease virus.
A:Reference number: S25642
A:Accession: S25642
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>
A:Cross-references: ENBL:X68392; NID:958687; PIDN:CAA48458.1; PID:958688
R:McClure, M.A.; Thibault, K.J.; Hataleki, C.G.; Lipkin, W.I.
J Virol. 66, 6572-6577, 1992
A>Title: Sequence similarity between Borna disease virus p40 and a duplicated domain w
A:Reference number: A44004; MUID:93021385; PMID:1404604
A:Accession: A44004
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 14-46, 'T', 48-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <MCC>
A:Cross-references: GB:M99375; NID:9210698; PIDN:AAA73385.1; PID:9210699
C:Superfamily: borna disease virus p40

Query Match 100.0%; Score 94; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.2e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:01:59 / Search time 134.727 Seconds
(without alignments)
51.672 Million cell updates/sec

Title: US-10-805-220-3

Perfect score: 94
Sequence: 1 PKRLVDADAMEDQDLY 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	18	AD575684	Ad575684 Borna dis
2	94	100.0	370	AAR98617	AAR98617 Borna dis
3	83	88.3	18	AAW49061	AAW49061 Human Bor
4	48	51.1	167	AB868561	AB868561 Drosophil
5	46	48.9	131	AAV66712	AAV66712 Membrane-
6	46	48.9	131	AAV57844	AAV57844 Human lep
7	46	48.9	131	AA803730	AA803730 OB-RGRP2
8	46	48.9	131	AA934849	AA934849 Human pro
9	46	48.9	131	AAU29127	AAU29127 Human mem
10	46	48.9	131	AA888337	AA888337 Human mem
11	46	48.9	131	AA85235	AA85235 Human PRO
12	46	48.9	131	AB89581	AB89581 Human pol
13	46	48.9	131	AB84894	AB84894 Human PRO
14	46	48.9	131	AB895500	AB895500 Human ang
15	46	48.9	131	ABU58503	ABU58503 Human PRO
16	46	48.9	131	ABU8051	ABU8051 Novel hum
17	46	48.9	131	ABU84366	ABU84366 Human sec
18	46	48.9	131	ABR66240	ABR66240 Human sec
19	46	48.9	131	ABR65630	ABR65630 Human sec
20	46	48.9	131	ABU99570	ABU99570 Human sec
21	46	48.9	131	ABU58050	ABU58050 Human PRO
22	46	48.9	131	ABU59128	ABU59128 Novel hum
23	46	48.9	131	ABU26640	ABU26640 Human sec
24	46	48.9	131	ABU2809	ABU2809 Human PRO
25	46	48.9	131	ABU89930	ABU89930 Novel hum

26	46	48.9	131	6	ABR68179	Human sec
27	46	48.9	131	6	ABU60559	Human sec
28	46	48.9	131	6	ABU96232	Novel hum
29	46	48.9	131	6	ABU92663	Human sec
30	46	48.9	131	6	ABO08740	Human sec
31	46	48.9	131	6	ABO02792	Human sec
32	46	48.9	131	6	ABR74946	Human sec
33	46	48.9	131	6	ABR94708	Human sec
34	46	48.9	131	6	ABU13941	Human PRO
35	46	48.9	131	6	ABU85681	Human PRO
36	46	48.9	131	6	ABU98841	Novel hum
37	46	48.9	131	6	ABU98056	Novel hum
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ALIGNMENTS

RESULT 1
AD575684
ID AD575684 standard; peptide; 18 AA.
XX
AC AD575684;
XX
DT 02-DEC-2004, (first entry)
XX
DE Borna disease virus p40 protein fragment #1 for detecting BDV infections.
XX
KW detection; exogenous antigen; class switching; IgM; IgG; immunoglobulin;
KW BDV; Borna disease virus; p24.
XX
OS Borna disease virus.
XX
PN EP1460426-A1.
XX
PD 22-SEP-2004.
XX
PF 19-MAR-2004; 2004EP-00006699.
XX
PR 20-MAR-2003; 2003JP-00078898.
PR 26-MAR-2003; 2003JP-00086490.
PR 26-MAR-2003; 2003JP-00086491.
(SYSM-) SYSMEX CORP.
Yamaguchi K, Horii Y, Takahama Y, Nagai S;
WPI; 2004-679696/57.
Detecting antibody against exogenous antigen e.g. Borna disease virus (BDV), involves detecting the IgM antibody to the exogenous antigen.
Claim 14; SEQ ID NO 3; 33pp; English.

The invention relates to a method of detecting (M1) an antibody, where an examination of a disease caused by an exogenous antigen is conducted, the exogenous antigen being an antigen having a property in which the class switching from the IgM antibody to the IgG antibody of immunoglobulin antibodies raised against the antigen is achieved after two months following the appearance of the IgM antibody, the method involves detecting the IgM antibody to the exogenous antigen. The specification also discloses a reagent (I) for detecting an anti-BDV antibody, the CC comprising an antigen polypeptide selected from the p10 region of a Borna disease virus (BDV) protein. (M1) is useful for detecting an antibody specific to an exogenous antigen. The exogenous antigen is a microorganism, virus and/or proteinaceous substance, which may be the

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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:27:58 ; Search time 103.182 Seconds
(without alignments)
60.826 Million cell updates/sec

Title: US-10-805-220-1

Perfect score: 77
Sequence: 1 QPVDQLLKDLRNKPS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	77	100.0	201	US-10-627-141-20	Sequence 20, Appl
3	77	100.0	201	US-10-627-141-20	Sequence 21, Appl
4	77	100.0	201	US-10-627-141-22	Sequence 22, Appl
5	50	64.9	456	US-09-978-360A-523	Sequence 523, Appl
6	49.5	64.3	420	US-11-097-143-4287	Sequence 4287, Ap
7	47	61.0	215	US-10-425-115-344991	Sequence 344991, A
8	45	58.4	129	US-10-767-701-37922	Sequence 37922, A
9	44	57.1	93	US-10-424-599-227834	Sequence 227834,
10	44	57.1	189	US-10-424-599-215846	Sequence 215846,
11	44	57.1	677	US-10-425-115-282920	Sequence 282920,

12	57.1	860	18	US-10-745-237-384	Sequence 384, App
13	57.1	1294	16	US-10-425-115-281171	Sequence 281171,
14	57.1	1386	16	US-10-476-924-2	Sequence 2, Appl1
15	55.8	63	15	US-10-335-977-5712	Sequence 5712, Ap
16	55.8	90	16	US-10-425-115-289813	Sequence 289813,
17	55.8	213	15	US-10-264-049-4344	Sequence 4344, Ap
18	55.8	287	16	US-10-425-115-241171	Sequence 241171,
19	55.8	664	15	US-10-372-683-39	Sequence 39, Appl
20	55.8	664	16	US-10-741-601-543	Sequence 543, App
21	55.8	664	16	US-10-741-601-544	Sequence 544, App
22	55.8	664	17	US-10-741-600-1568	Sequence 1568, Ap
23	55.8	664	17	US-10-741-600-1569	Sequence 1569, Ap
24	55.8	684	9	US-09-925-302-555	Sequence 555, App
25	55.8	684	10	US-09-925-302-555	Sequence 555, App
26	55.8	895	14	US-10-032-585-7321	Sequence 7321, Ap
27	55.8	895	17	US-10-732-923-22452	Sequence 22452, A
28	55.8	1030	15	US-10-282-122A-68934	Sequence 68934, A
29	55.8	2047	16	US-10-437-963-196733	Sequence 196733,
30	55.8	4498	17	US-10-732-923-15008	Sequence 15008, A
31	54.5	148	20	US-11-097-143-3072	Sequence 3072, Ap
32	54.5	338	16	US-10-739-930-9663	Sequence 9663, Ap
33	54.5	445	15	US-10-369-493-619	Sequence 619, App
34	54.5	445	17	US-10-732-923-1041	Sequence 1041, Ap
35	54.5	917	20	US-11-034-275-27	Sequence 27, Appl
36	54.5	1113	16	US-10-437-963-110624	Sequence 110624,
37	54.5	1359	16	US-10-437-963-110622	Sequence 110622,
38	54.5	1810	20	US-11-097-143-3738	Sequence 3738, Ap
39	53.2	192	15	US-10-291-265-261	Sequence 261, App
40	53.2	520	15	US-10-425-114-47284	Sequence 47284, A
41	53.2	542	18	US-10-450-763-48073	Sequence 48073, A
42	53.2	556	15	US-10-369-493-750	Sequence 750, App
43	53.2	570	15	US-10-424-599-240986	Sequence 240986,
44	53.2	606	18	US-10-450-763-48075	Sequence 48075, A
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10805220
; Publication No. US20040234955A1
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, Kazunari
; APPLICANT: HORII, Yoichiro
; APPLICANT: TAKAHAMA, Youichi
; APPLICANT: NAGAI, Shinya
; TITLE OF INVENTION: METHOD FOR DETECTING ANTIBODY AND ANTIGEN FOR DETECTING BORNA DISEASE VIRUS
; FILE REFERENCE: Q80490
; CURRENT APPLICATION NUMBER: US/10/805,220
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: JPA 2003-078898
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JPA 2003-086490
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: JPA 2003-086491
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Borna disease virus
US-10-805-220-1

Query Match 100.0%; Score 77; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPVDQLLKDLRNKPS 15
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OM protein - protein search, using sw model

Run on: November 3, 2005, 15:21:48 ; Search time 27.7273 Seconds
(without alignments)
40.384 Million cell updates/sec

Title: US-10-805-220-1

Perfect score: 77

Sequence: 1 QPVDQLKDLKRNPS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	77	100.0	201	3	US-08-779-764A-22
5	77	100.0	201	3	US-08-582-776C-4
6	77	100.0	201	3	US-08-434-831B-4
7	77	100.0	201	4	US-09-563-456-20
8	77	100.0	201	4	US-09-563-456-21
9	77	100.0	201	4	US-09-563-456-22
10	49.5	64.3	159	4	US-09-270-767-45877
11	43	55.8	664	1	US-08-421-661-6
12	43	55.8	664	4	US-09-917-254-78
13	43	55.8	709	4	US-09-949-016-10367
14	41	53.2	355	4	US-09-543-681A-4641
15	41	53.2	385	4	US-09-107-532A-4972
16	41	53.2	727	4	US-09-540-236-3023
17	40	51.9	12	3	US-08-582-776C-21
18	40	51.9	12	3	US-08-434-831B-21
19	40	51.9	387	4	US-09-270-767-44830
20	40	51.9	468	4	US-09-248-796A-17456
21	39	50.6	370	3	US-09-134-001C-3769
22	39	50.6	551	4	US-09-540-236-2436
23	39	50.6	800	3	US-08-776-265-3
24	39	50.6	800	4	US-09-398-184-3
25	39	50.6	886	4	US-08-956-171E-5235
26	39	50.6	886	4	US-08-781-986A-5235
27	38	49.4	67	4	US-09-248-796A-21695

28	38	49.4	67	4	US-09-248-796A-23806	Sequence 23806, A
29	38	49.4	100	2	US-08-710-249-16	Sequence 16, Appl
30	38	49.4	100	3	US-09-220-157A-16	Sequence 16, Appl
31	38	49.4	150	4	US-09-248-796A-25579	Sequence 25579, A
32	38	49.4	308	4	US-09-584-568C-8	Sequence 8, Appl
33	38	49.4	316	4	US-09-248-796A-16753	Sequence 16753, A
34	38	49.4	347	4	US-09-710-279-462	Sequence 462, App
35	38	49.4	347	4	US-09-710-279-462	Sequence 462, App
36	38	49.4	351	3	US-09-134-001C-5492	Sequence 1268, Ap
37	38	49.4	380	4	US-09-254-776B-80	Sequence 5492, Ap
38	38	49.4	503	4	US-09-198-452A-263	Sequence 80, Appl
39	38	49.4	506	2	US-08-659-984A-21	Sequence 263, App
40	38	49.4	506	3	US-08-660-531-21	Sequence 21, Appl
41	38	49.4	506	3	US-09-054-334-4	Sequence 21, Appl
42	38	49.4	508	4	US-09-438-185A-253	Sequence 253, App
43	38	49.4	510	3	US-09-522-217-89	Sequence 89, Appl
44	38	49.4	510	4	US-09-923-246-89	Sequence 89, Appl
45	38	49.4	510	4	US-10-295-723-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-08-369-822C-4
; Sequence 4, Application US/08369822C
; Patent No. 6015660
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. I.
; APPLICANT: Briese, Thomas
; APPLICANT: Kliche, Stefanie
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Stitz, Lothar
; APPLICANT: Schneemann, Anette
; TITLE OF INVENTION: Borna Disease Viral Sequences,
; TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fulbright & Jaworski, L.L.P.
; STREET: 865 South Figueroa Street, 29th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017-2571
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
; SOFTWARE: ASCII (DOS) TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,822C
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Churchill, Margaret A. (Ph.D.)
; REGISTRATION NUMBER: 39,944
; REFERENCE/DOCKET NUMBER: 1279-194XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213/892-9200
; TELEFAX: 213/680-4518
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-369-822C-4

Query Match 100.0%; Score 77; DB 3; Length 201;